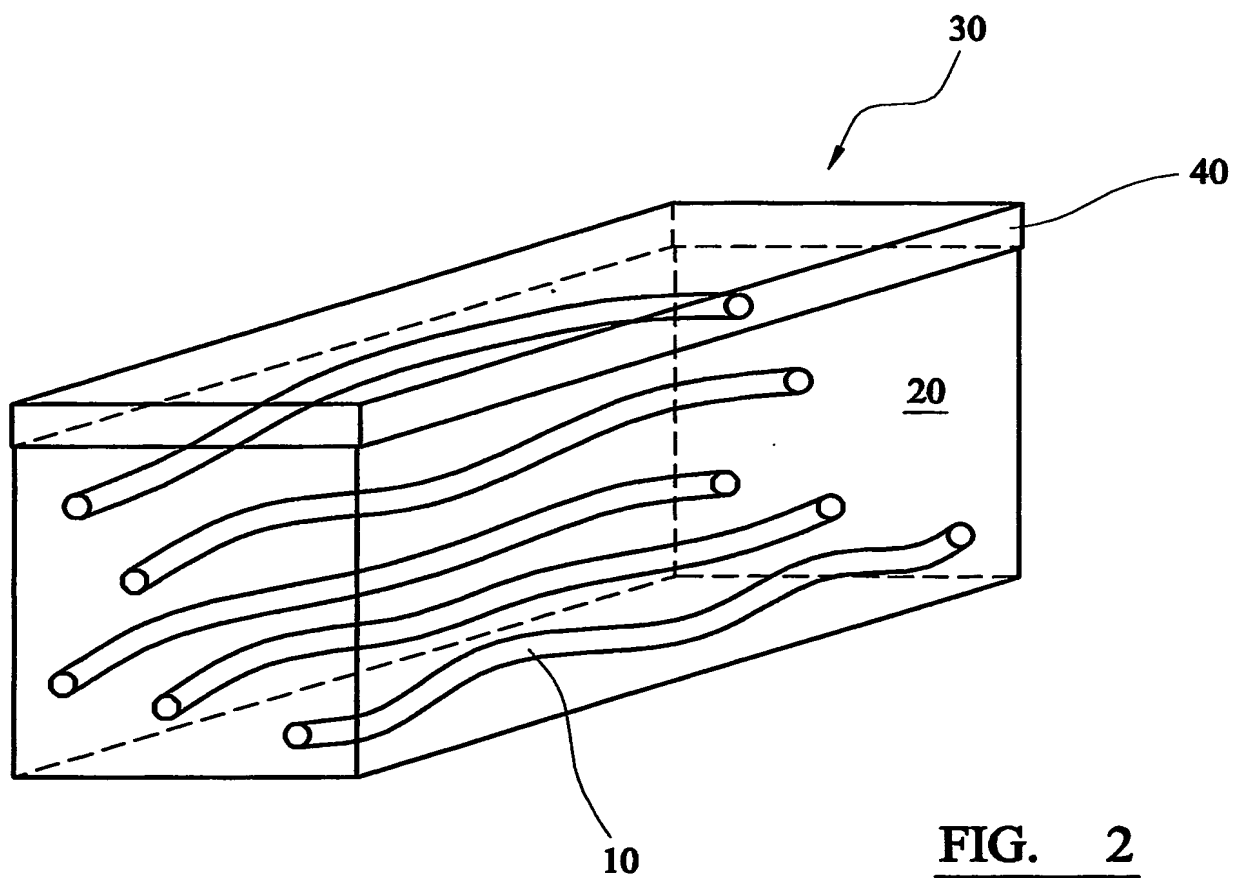
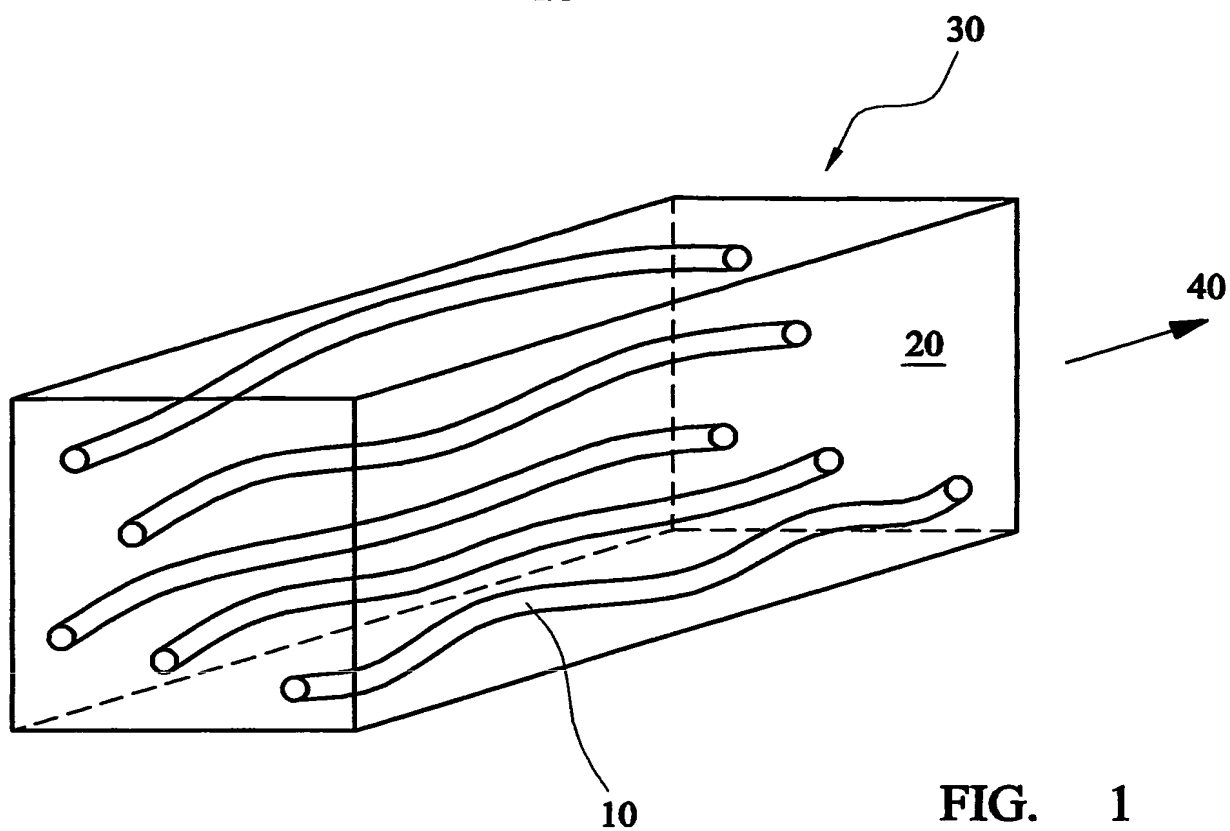


-1/5-



-2/5-

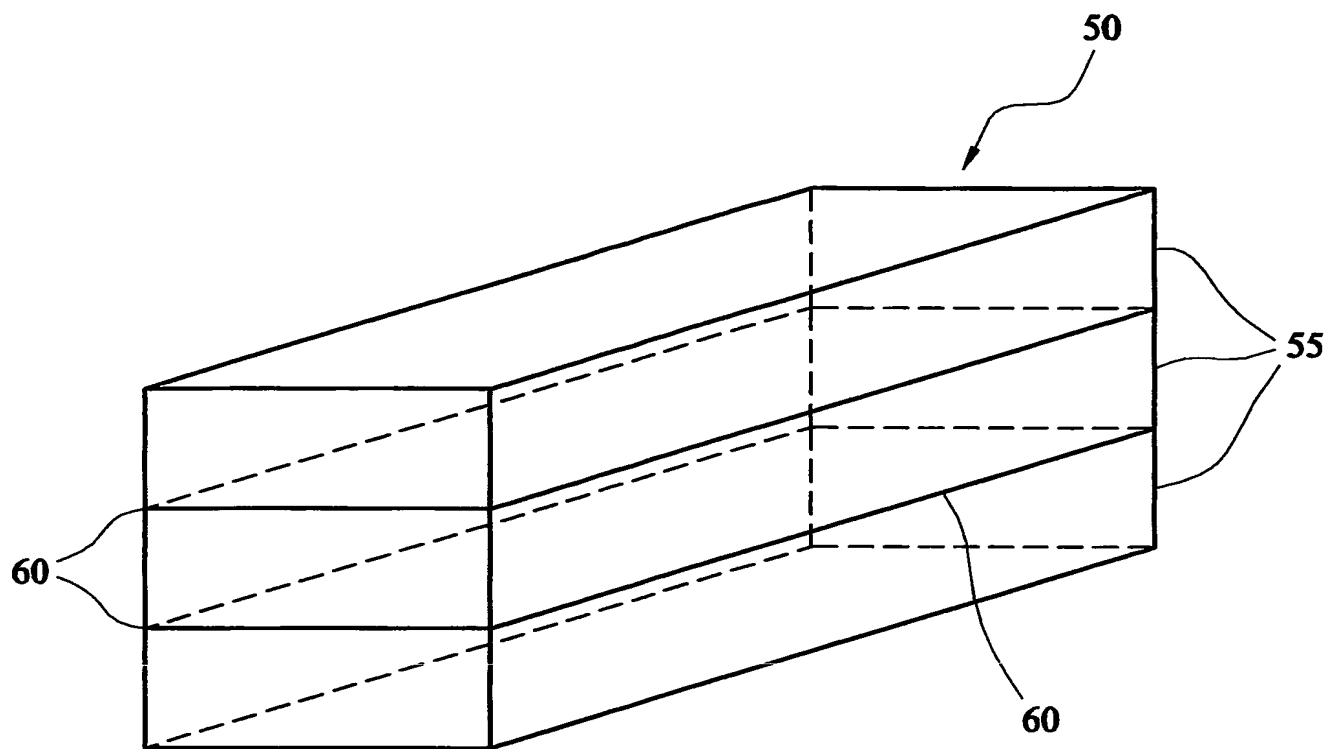


FIG. 3

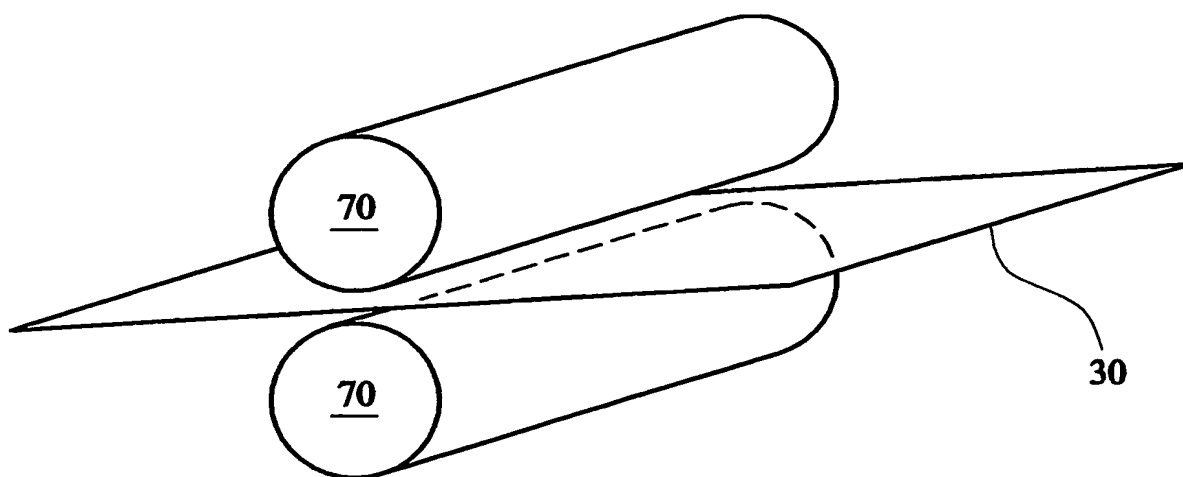


FIG. 4

-3/5-

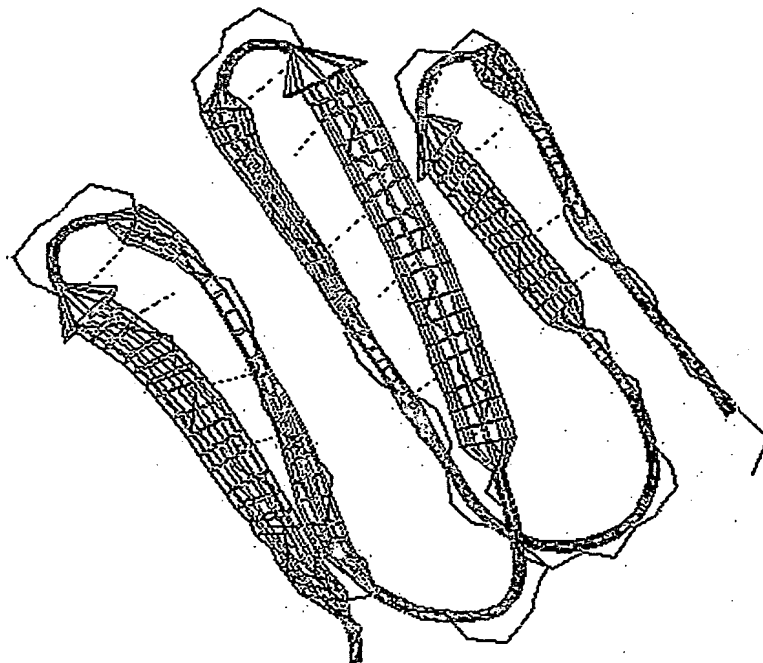
## Consensus repeat structure of sericin precursor protein

No. of Repeats	Total Score	Length	Diagonal	BW-From	BW-To	Level
7	529.97	35	35	317	351	1

131-	164	(46.31/ 7.35)	SSSSSTeeSS...SSSR..AASSTDASNTDSNSNSA
165-	202	(82.44/20.60)	GSSTSGG..RRTYGYSSNSRDGSVSSSTGSSSENTDSNSNSA
203-	240	(83.27/20.91)	GSSTSGG..SSTYGYSSNSRDGSVSTTGSSSENTDSNSNSV
241-	278	(68.12/15.35)	GSRRSGG..SSSHEDSSKARDENVBTGSSSENTDSNSNSV
279-	316	(82.44/20.60)	GSSTSGG..RRTYGYSSNSRDGSVSSSTGSSSENTDSNSNSV
317-	354	(84.15/21.23)	GSSTSGG..SSTYGYSSNSRDGSVSSSTGSSSENTDSNSNSA
355-	389	(83.23/20.90)	GSSTSGG..SSTYGYSSNSHDGSVSSSTGSSSENTDSNS

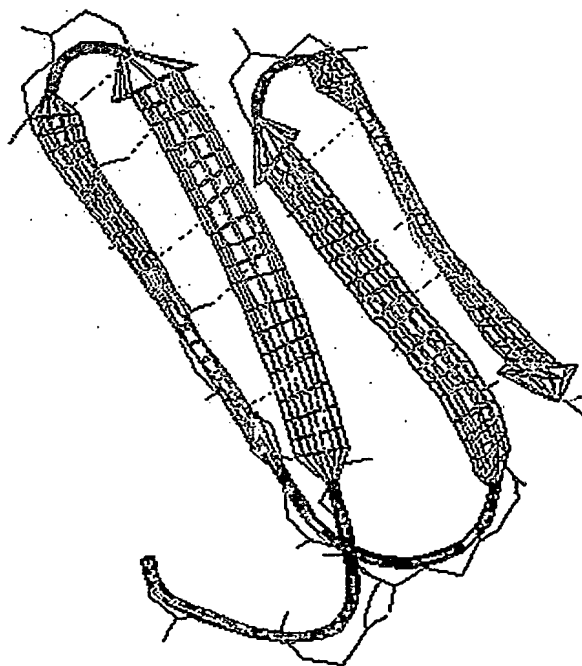
FIG. 5

-4/5-



**Ice nucleation protien (inaz) from the published PDB file**

**FIG. 6**



**Swiss model for consensus sequence of sericin precursor protein using  
inaz as a template**

**FIG. 7**

-5/5-

The best LALIGN alignment of sericin precursor protein with INAC.

24.4% identity in 336 aa overlap; score: 265 E(10,000): 4.9e-16

	500	510	520	530	540	550
INAZ	STGTAGADSSLIAGYGSTQTSGSESSLTAGYGSTQTAREGSTLTAGYGSTGTAGADSSLI					
	: . . . : : . : : : : : : : : : : . . . . . : . . . . .					
serici	SAGAHRAKSVEQSQDKSKYTSQPEGVSTSGRSQNYKDSKQAIISGGTKSSNSNVQSDEKS					
	60	70	80	90	100	110

	560	570	580	590	600	610
INAZ	AGYGSTQTSGSESSLTAGYGSTQTAQQGSVLTSYGSTQTAGAASNLTGYGSTGTAGHE					
	: . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .					
serici	ASQSSSRSSQESASYSSSSSSSTEESSSSSRAASSTDASSNTDSNSNSAGSSTSGGRR					
	120	130	140	150	160	170

	620	630	640	650	660	670
INAZ	SFIIAGY---GSTQTAGHKSILTAGYGSTQTARDGSDLIAGYGSTGTAGS----GSSLIA					
	. . . : . . . . : : . . . . . : . . . . . : . . . . . : . . . . .					
serici	TYGYSSNSRDGVSSTGSSSNTDSNSSNAGSSTSGGSSTYGYSSNSRDGVSSTGSSSNT					
	180	190	200	210	220	230

	680	690	700	710	720	730
INAZ	GYGSTQTASYRSMILTAGYGSTQTAREHSDLVTGYGSTSTAGSNSSLIAGYGSTGTAGFKS					
	: . . . . : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .					
serici	DSNSNSVGSRRSGSSSHEDSSKSRDENVTGSSSNTDSNSNSVGSSTSGGRRRTYGYSS					
	240	250	260	270	280	290

**FIG. 8**